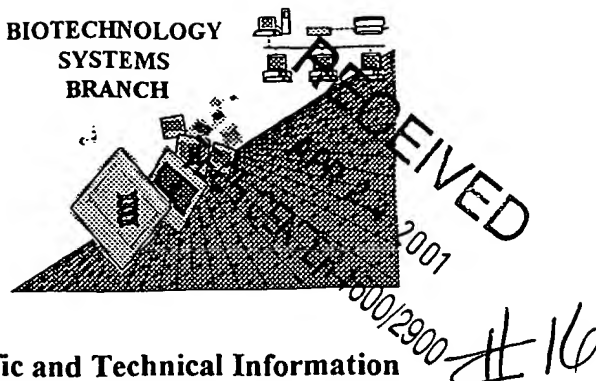# RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/430,735A_

Source: _1627_

Date Processed by STIC: _4/13/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

G. Hsu (handwritten signature, top left)

1627

RAW SEQUENCE LISTING   DATE: 04/13/2001
PATENT APPLICATION: US/09/430,735A   TIME: 13:19:17

Input Set : A:\9233-8DV2.txt
Output Set: N:\CRF3\04122001\I430735A.raw

PP. 1-5 (handwritten)

Does Not Comply Corrected Diskette Needed (handwritten)

```
 3 <110> APPLICANT: Ekwuribe, Nnochiri
 4        Radhakrishnan, Balasingam
 5        Price, Christopher
 6        Anderson, Wesley
 7        Ansari, Aslam
 9 <120> TITLE OF INVENTION: METHODS FOR INDUCING ANALGESIA
11 <130> FILE REFERENCE: 9233.8DV2
13 <140> CURRENT APPLICATION NUMBER: 09/430,735A
14 <141> CURRENT FILING DATE: 1999-10-29
16 <150> PRIOR APPLICATION NUMBER: 09/134,803
17 <151> PRIOR FILING DATE: 1998-08-14
19 <160> NUMBER OF SEQ ID NOS: 52
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 6
25 <212> TYPE: PRT
26 <213> ORGANISM: synthetic construct
28 <220> FEATURE:
29 <221> NAME/KEY: MOD_RES
30 <222> LOCATION: (6)..(6)
31 <223> OTHER INFORMATION: Polymer connected to epsilon-amino group
34 <400> SEQUENCE: 1
36 Tyr Gly Gly Phe Met Lys
37 1               5
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 6
41 <212> TYPE: PRT
42 <213> ORGANISM: synthetic construct
44 <220> FEATURE:
45 <221> NAME/KEY: MOD_RES
46 <222> LOCATION: (1)..(1)
47 <223> OTHER INFORMATION: Polymer connected to alpha-amino group
50 <220> FEATURE:
51 <221> NAME/KEY: MOD_RES
52 <222> LOCATION: (6)..(6)
53 <223> OTHER INFORMATION: Polymer connected to epsilon-amino group
56 <400> SEQUENCE: 2
58 Tyr Gly Gly Phe Met Lys
59 1               5
61 <210> SEQ ID NO: 3
62 <211> LENGTH: 6
63 <212> TYPE: PRT
64 <213> ORGANISM: synthetic construct
66 <220> FEATURE:
67 <221> NAME/KEY: MOD_RES
68 <222> LOCATION: (1)..(1)
69 <223> OTHER INFORMATION: Polymer connected to alpha-amino group
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(handwritten note, right side): Per 1.823 of new Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species) (one of the three) (see circled portion of item 12 on Error Summary Sheet)

```
                RAW SEQUENCE LISTING              DATE: 04/13/2001
                PATENT APPLICATION: US/09/430,735A    TIME: 13:19:17

                Input Set : A:\9233-8DV2.txt
                Output Set: N:\CRF3\04122001\I430735A.raw

 72  <400> SEQUENCE: 3
 74  Tyr Gly Gly Phe Met Lys
 75  1                   5
 77  <210> SEQ ID NO: 4
 78  <211> LENGTH: 6
 79  <212> TYPE: PRT
 80  <213> ORGANISM: synthetic construct
 82  <220> FEATURE:
 83  <221> NAME/KEY: MOD_RES
 84  <222> LOCATION: (1)..(1)
 85  <223> OTHER INFORMATION: ACETYLATION
 88  <220> FEATURE:
 89  <221> NAME/KEY: MOD_RES
 90  <222> LOCATION: (6)..(6)
 91  <223> OTHER INFORMATION: AMIDATION
 94  <400> SEQUENCE: 4
 96  Phe Arg Trp Trp Tyr Lys
 97  1                   5
 99  <210> SEQ ID NO: 5
100  <211> LENGTH: 6
101  <212> TYPE: PRT
102  <213> ORGANISM: synthetic construct
104  <220> FEATURE:
105  <221> NAME/KEY: MOD_RES
106  <222> LOCATION: (1)..(1)
107  <223> OTHER INFORMATION: ACETYLATION
110  <220> FEATURE:
111  <221> NAME/KEY: MOD_RES
112  <222> LOCATION: (6)..(6)
113  <223> OTHER INFORMATION: AMIDATION
116  <400> SEQUENCE: 5
118  Arg Trp Ile Gly Trp Lys
119  1                   5
121  <210> SEQ ID NO: 6
122  <211> LENGTH: 6
123  <212> TYPE: PRT
124  <213> ORGANISM: synthetic construct
126  <220> FEATURE:
127  <221> NAME/KEY: MOD_RES
128  <222> LOCATION: (6)..(6)
129  <223> OTHER INFORMATION: AMIDATION
132  <220> FEATURE:
133  <221> NAME/KEY: UNSURE
134  <222> LOCATION: (6)..(6)
135  <223> OTHER INFORMATION: Xaa can be any of the twenty naturally occurring amino acids
138  <400> SEQUENCE: 6
140  Trp Trp Pro Lys His Xaa
141  1                   5
143  <210> SEQ ID NO: 7
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```
             RAW SEQUENCE LISTING              DATE: 04/13/2001
             PATENT APPLICATION:  US/09/430,735A      TIME: 13:19:17

             Input Set : A:\9233-8DV2.txt
             Output Set: N:\CRF3\04122001\I430735A.raw

  144 <211> LENGTH: 4
  145 <212> TYPE: PRT
  146 <213> ORGANISM: synthetic construct
  148 <220> FEATURE:
  149 <221> NAME/KEY: MOD_RES
  150 <222> LOCATION: (4)..(4)
  151 <223> OTHER INFORMATION: AMIDATION
  154 <220> FEATURE:
  155 <221> NAME/KEY: UNSURE
  156 <222> LOCATION: (4)..(4)
  157 <223> OTHER INFORMATION: Xaa is either Lys or Arg
  160 <400> SEQUENCE: 7
  162 Trp Trp Pro Xaa
  163 1
  165 <210> SEQ ID NO: 8
  166 <211> LENGTH: 6
  167 <212> TYPE: PRT
  168 <213> ORGANISM: synthetic construct
  170 <220> FEATURE:
  171 <221> NAME/KEY: MOD_RES
  172 <222> LOCATION: (6)..(6)
  173 <223> OTHER INFORMATION: AMIDATION
  176 <220> FEATURE:
  177 <221> NAME/KEY: UNSURE
  178 <222> LOCATION: (6)..(6)
  179 <223> OTHER INFORMATION: Xaa can be any one of the naturally occurring amino acids
  182 <400> SEQUENCE: 8
  184 Tyr Pro Phe Gly Phe Xaa
  185 1               5
  187 <210> SEQ ID NO: 9
  188 <211> LENGTH: 7
  189 <212> TYPE: PRT
  190 <213> ORGANISM: synthetic construct
  192 <220> FEATURE:
  193 <221> NAME/KEY: MOD_RES
  194 <222> LOCATION: (1)..(5)
  195 <223> OTHER INFORMATION: Amino acids are in the D-form
  198 <220> FEATURE:
  199 <221> NAME/KEY: MOD_RES
  200 <222> LOCATION: (6)..(6)
  201 <223> OTHER INFORMATION: n is 0 or 1
  204 <220> FEATURE:
  205 <221> NAME/KEY: MOD_RES
  206 <222> LOCATION: (7)..(7)
  207 <223> OTHER INFORMATION: Xaa is Gly or the D-form of a naturally occurring amino acid
  210 <220> FEATURE:
  211 <221> NAME/KEY: MOD_RES
  212 <222> LOCATION: (7)..(7)
  213 <223> OTHER INFORMATION: AMIDATION
```

```
216 <400> SEQUENCE: 9
218 Ile Met Ser Trp Trp Gly Xaa
219 1                   5
221 <210> SEQ ID NO: 10
222 <211> LENGTH: 6
223 <212> TYPE: PRT
224 <213> ORGANISM: synthetic construct
226 <220> FEATURE:
227 <221> NAME/KEY: MOD_RES
228 <222> LOCATION: (1)..(4)
229 <223> OTHER INFORMATION: Amino acids are in the D-form
232 <220> FEATURE:
233 <221> NAME/KEY: MOD_RES
234 <222> LOCATION: (6)..(6)
235 <223> OTHER INFORMATION: Xaa is Gly or the D-form of a naturally-occurring amino acid
238 <220> FEATURE:
239 <221> NAME/KEY: MOD_RES
240 <222> LOCATION: (6)..(6)
241 <223> OTHER INFORMATION: AMIDATION
244 <400> SEQUENCE: 10
246 Ile Met Thr Trp Gly Xaa
247 1                 5
249 <210> SEQ ID NO: 11
250 <211> LENGTH: 4
251 <212> TYPE: PRT
252 <213> ORGANISM: synthetic construct
254 <220> FEATURE:
255 <221> NAME/KEY: MOD_RES
256 <222> LOCATION: (2)..(2)
257 <223> OTHER INFORMATION: Xaa is A1, wherein A1 is the D-form of Nve or Nle
260 <220> FEATURE:
261 <221> NAME/KEY: MOD_RES
262 <222> LOCATION: (3)..(3)
263 <223> OTHER INFORMATION: Xaa is B2, wherein B2 is Gly, Phe, or Trp
266 <220> FEATURE:
267 <221> NAME/KEY: MOD_RES
268 <222> LOCATION: (4)..(4)
269 <223> OTHER INFORMATION: Xaa is C3, wherein C3 is Trp or Nap
272 <220> FEATURE:
273 <221> NAME/KEY: MOD_RES
274 <222> LOCATION: (4)..(4)
275 <223> OTHER INFORMATION: AMIDATION
278 <400> SEQUENCE: 11
280 Tyr Xaa Xaa Xaa
281 1
283 <210> SEQ ID NO: 12
284 <211> LENGTH: 3
285 <212> TYPE: PRT
286 <213> ORGANISM: synthetic construct
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```
        RAW SEQUENCE LISTING                 DATE: 04/13/2001
        PATENT APPLICATION:  US/09/430,735A   TIME: 13:19:17

        Input Set : A:\9233-8DV2.txt
        Output Set: N:\CRF3\04122001\I430735A.raw

288 <220> FEATURE:
289 <221> NAME/KEY: MOD_RES
290 <222> LOCATION: (1)..(1)
291 <223> OTHER INFORMATION: Tyr has at its N-terminus an Me-x-H-y-N group, wherein x is 0, 1,
292      or 2; and y is 0, 1, or 2, with the proviso that x and y is neve
293      r greater than  What? (incomplete response)
296 <220> FEATURE:
297 <221> NAME/KEY: MOD_RES
298 <222> LOCATION: (1)..(2)
299 <223> OTHER INFORMATION: The amine between the first Tyr and the second Tyr is methylated
303 <220> FEATURE:
304 <221> NAME/KEY: MOD_RES
305 <222> LOCATION: (3)..(3)
306 <223> OTHER INFORMATION: Xaa is Xaa-z, wherein Xaa is Phe, (D)Phe, or NHBzl and wherein z
307      is 0 or ? (what)
310 <220> FEATURE:
311 <221> NAME/KEY: MOD_RES
312 <222> LOCATION: (3)..(3)
313 <223> OTHER INFORMATION: AMIDATION
316 <400> SEQUENCE: 12
318 Tyr Tyr Xaa
319 1
321 <210> SEQ ID NO: 13
322 <211> LENGTH: 6
323 <212> TYPE: PRT
324 <213> ORGANISM: synthetic construct
326 <220> FEATURE:
327 <221> NAME/KEY: MOD_RES
328 <222> LOCATION: (4)..(4)
329 <223> OTHER INFORMATION: Xaa is D4, wherein D4 is Lys or Arg
332 <220> FEATURE:
333 <221> NAME/KEY: MOD_RES
334 <222> LOCATION: (5)..(5)
335 <223> OTHER INFORMATION: His is His-z, wherein z is 0 or 1
338 <220> FEATURE:
339 <221> NAME/KEY: MOD_RES
340 <222> LOCATION: (6)..(6)
341 <223> OTHER INFORMATION: Xaa is Xaa-z, wherein Xaa is a naturally occurring amino acid and
342      z is 0 or what?
345 <220> FEATURE:
346 <221> NAME/KEY: MOD_RES
347 <222> LOCATION: (6)..(6)
348 <223> OTHER INFORMATION: AMIDATION
351 <400> SEQUENCE: 13
W--> 353 Trp Trp Pro Xaa His Xaa
354 1           . 5
356 <210> SEQ ID NO: 14
357 <211> LENGTH: 4
358 <212> TYPE: PRT
```

[Handwritten annotations:]
FYI: Xaa can only represent a single amino acid, nothing else

Please correct this error in subsequent sequence.

Please ensure all subsequent <223 responses are complete.

Please Not :
Us of n and/or Xaa have been detected in the S qu nce Listing. Please review the
Sequence Listing to ensure that a corresp nding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 04/13/2001
PATENT APPLICATION: US/09/430,735A   TIME: 13:19:18

Input Set : A:\9233-8DV2.txt
Output Set: N:\CRF3\04122001\I430735A.raw

```
L:140  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:162  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:184  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:218  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:246  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:280  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:318  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:353  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:369  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:391  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:413  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:435  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:457  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:479  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:501  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:529  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:551  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:573  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:595  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:624  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:659  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:682  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:705  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:734  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:756  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:772  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:794  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:810  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:832  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:854  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:876  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:898  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:920  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:942  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:964  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:986  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1080 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:1103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
```

~~   CProject   ~~

 CProjectData   -METHODS FOR INDUCING ANALGESIA   9233.8DV2
09/430,735
1999-10-29   4   ~~   CProtein1Sequence   seq1 synthetic
construct YGGFMK   ARNDBCQEZGHILKMFPSTWYVX   PRT   ~~
    CCommentFeature   ¦¦¦¦~~~~~~   COtherFeature   MOD_RES(Polymer
connected to epsilon-amino group 6 6   ?   seq2 synthetic
construct YGGFMK   ·   ARNDBCQEZGHILKMFPSTWYVX   PRT   ?
          ,   " -   ?
    MOD_RES&Polymer connected to alpha-amino group 1 1   ?
    MOD_RES(Polymer connected to epsilon-amino
group 6 6   ?   seq3 synthetic
construct YGGFMK   ARNDBCQEZGHILKMFPSTWYVX   PRT   ?
                 ?   MOD_RES&Polymer connected to alpha-amino
group 1 1   ?   SEQ 4 synthetic
construct FRWWYK   ARNDBCQEZGHILKMFPSTWYVX   PRT   ?
                 ?   MOD_RES   .
ACETYLATION 1 1   ?   MOD_RES
     AMIDATION 6 6   ?   S5 synthetic
construct RWIGWK   ARNDBCQEZGHILKMFPSTWYVX   PRT   ?
                 ?   MOD_RES
ACETYLATION 1 1   ?   MOD_RES
     AMIDATION 6 6   ?   S6 synthetic
construct WWPKHX   ARNDBCQEZGHILKMFPSTWYVX   PRT   ?
                 ?   MOD_RES   AMIDATION 6 6
     ?   UNSURE<Xaa can be any of the twenty naturally occurring amino
acids 6 6   ?   s7 synthetic
construct WWPX   ARNDBCQEZGHILKMFPSTWYVX   PRT   ?-
                 ?-   MOD_RES   AMIDATION 4 4

Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of "Artificial" (NEW RULES)

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001